

## TITLE: NUCLEIC ACID INTERGRATION IN EUKARYOTES

Inventor: Hooykaas et al.

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Fig. 1

Strain	LB' CAGGATATATTCAATTGTAAAT-CTC---CGA-GG RB'	Chromosome, coordinate and location
WT.51	<sup>-4</sup> 5' ATTGTATTATATATTCAATTGTAAAT-CTC---CGA-GGTA 3'	XIV, 185311 (1 bp of target site DNA deleted), int. region
<i>rad50k.1</i>	<sup>-6</sup> 5' TGTGGGTGTGATATTCAATTGTAAAT-CTC---CGA-GG 3'	XV, 1091277, tel. region
<i>rad50k.5</i>	<sup>-7</sup> 5' GGGGGCATCAGTATTCAATTGTAAAT-CTC---CGA-GG 3'	XII, 465986, rDNA region
<i>rad50k.6</i>	<sup>-25</sup> 5' GAGGTAGATGTGAGAGAGTGTGTGGGTGTGAAGTCGA 3'	XV, 1091276, tel. region
<i>mre11k.4</i>	<sup>-3</sup> 5' TCTGGTAGATATATTCAATTGTAAAT-CTC---CGA-GG 3'	XII, 459692/468829, rDNA region
<i>mre11k.5</i>	<sup>-8</sup> 5' CACATATTTCTCATTCAATTGTAAAT-CTC---CGA-GG 3'	VII/X/XIII, 536090 OR 541678/472487 OR 483659/196667, LTR
<i>mre11k.8</i>	<sup>-11</sup> 5' CGACTACTTTTATATCCAATTGTAAAT-CTC---CGA-GG 3'	XIV, 6060, subtel. region
<i>mre11k.11</i>	<sup>-7</sup> 5' GAAGAACCCATTATTCAATTGTAAAT-CTC---CGA-GG 3'	XIV, 4866, subtel. region
<i>mre11k.14</i>	<sup>-7</sup> 5' TGGGTGTGGGTATTCAATTGTAAAT-CTC---CGA-GG 3'	VIII, 562588, tel. region
<i>mre11k.17</i>	<sup>-9</sup> 5' TGGGTGTGGTGTGTCAATTGTAAAT-CTC---CGA-GG 3'	XII, 5727, subtel. region
<i>xrs2k.1</i>	<sup>-10</sup> 5' TGTGTGGGTGTGGGTCAATTGTAAAT-CTC---CGA-GG 3'	IX/X, 69/52, tel. region
<i>xrs2k.17</i>	<sup>-1</sup> 5' CGTCAAGGATATATTCAATTGTAAAT-CTC---CGA-GG 3'	XII, 1071797, subtel. region

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Fig. 2

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Sc 1 -----MRSVTNAFGNSGELNMGHESGYRKADLTCGAFCELSSETMFKESSALEYKSPILLEIESDEMSQLNTRP
Hs 1 MSGWESYYKTEGDEEAEFEQPCALASGDYKSGHPSLFLASKAMFESQSDLT-PFDMSLCCQOSYISKHLS
At 1 -----

Sc 75 GTATCYEYYCNDAKEGIYEPIRLNATFMKENDLLEDLSSGRISLYDFMFQQTGSEKQRLSVLTFELDTFL
Hs 80 RDLAVVEYGTENKNSVNFKNFVLOADNPGANLLELDQFKGQOGQKRODMMGHGSYSL-SEVLVVCANLF
At 1 -----

Sc 155 EAPGCKQSNKRFLETFIDKEQEAQD-IDERARLER---LTIDLFNKNFATFFGYADKPDN-EFYSDIOLASH
Hs 155 SLP--CFKSHKRLFTNEDNEHGND--SAKASART---FAGDLRTGTGFLEHLKKPGG-FDILFYDIISLE-
At 16 RKG--SLKTEDKRFLETFNEDDEFGSMRISVNEDMTETILOAKAQILGISLPLPSOPDQENILFYDAIGLS-

Sc 230 TIENTGLDEFDGPSKPKAKYFESHLENKEVKRIFFQCPLEIDKTNFAGVKGTYTTEKASVRYKSEHEHIR
Hs 226 -DE---DLRVHFEDSKLEL--ALR--ANETRKRA--SRK--KLNKD--FISVGINLROGKPP---PKLYRFTN
At 93 -DE---LLEEMPSVGQKLED--RDO--AVLAKRIAKRITFCG--SLEENGVALRPAFES---ETEDSTIN

Sc 310 QEAYKRENNPITG-EDTGGKIVFHYBYGOLDINLEDSQDI MEAYTQDFFLGGFSSSKSEYNNNDKSEFIV
Hs 294 EPVRATFTNTSTGGLPSDTRKRSCHYGRGISEKEETEEKRFD---DFGLMLGFKPLV-LKKHHYLPSEIFY
At 161 LPVKVERSGCTDTG-AADQPIORTOPYKNOIFVVEELSOVKRIS---THLLELGFKPLS-CLNDHNLPSIFY

Sc 389 PFAKYEGSIRTLAELLIRKRIALNGKLSNHHESLYTLPSS--KADYN---EGFYTYRPFELDIRKPSL
Hs 370 PLESVIGSSTLFSALLIKCEKEVAACRYTPRNIPYFVALVPOEE--LQKIQVTPPGFLLLPFADDKRF---
At 236 PSEKEVIGSRAFIALHSSIOLEFAFANG--GTPPERLVALVAC--EASDGGQVBPGEITSLPANDIRDEL

Sc 462 LSYDDGSEKDYDNMKVVTQIMGYFNLDCYNPSDEKNPLQXHYALHDYLL---METTFDENETPNTRKES---
Hs 447 ---PEFENIATPQCGMKATEELRFT--YRSDSEENPLQCHENLEAALDLMEPEQAVCLLPKVERINE-RIG
At 313 HSK-PGVAXPRA--DAQKKASAMRELELE--SVCOFANPALORHYANLOALDENE--RETRCETLPDEE--MNEPAW

Sc 537 EEDDSLKLYYYIRKIDES-----FSEDPIIORLNKYVKIWN-----MFYKKN-----DDNSKKEEK
Hs 520 SLDETFRELYPPDYNPBGK-VTKRHDNEGSGSKRP-EVEYSEELKTHISKCTLGKFTVPMLEACRAYGLKSGLRKQ
At 391 EALLOEKQSYGDDPDEESGAKENSKKRKAGDADDGYIYIEL-AKT---GKLEDLTVVELETYLTANNLISGRKE

Sc 593 PFDKPKFNI--
Hs 598 ELDEATKRFQD
At 466 VLENALTLTGK

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Fig. 3A

Sc 1 MISALDSPEPQNFAPSPDFKWFCEELVVKTHEVQINGTAGGKSSFKYVEIISNVEMWRKTVGNNTYEALVLALPYE  
Hs 1 -----LTFPLM-----  
At 1 -----LTFPLM-----

Sc 81 RRRINIKYVLIETCSYLKLPASATEORLKQV--QRVGRGNLS--SLVEETARRAEPSSKRTIDVNHLYDS  
Hs 11 ERMAYGIKEMLARLYTLLNLPRDEKDALLLNR--TPTGTHGAGDFRIAYEVLRPF--CLQKSLTIQVNDLLDS  
At 57 ERGSYGIKEVVLATCITGALGSRDPDARLLNWRKGGTAKAGNAGNFSLIAAEVLORROGASGLTIKEINDLLR

Sc 157 LGDRFASGRFKZLVKSKPFLHCEEMSEVEKRFDDILNRVIGGCEKILCCHPDACVLSVLDLNVTSRLYE  
Hs 88 IASN---NSAKRKDLKKR--LIGLETSSATEORLIRIRLDLKLGS--QIFSVFHNDAAHLNVTDIEKVCROLAC  
At 137 LASS---ENRERLVLSS--LQKTN---AOKKWRIRIILDKLKLGS--QIFSEHPDAEDLNVTCDLKTVCEKLC

Sc 237 PVRLKDDDSIKVGFAPAPOLAKENLSYEKICETLHDDFVEERDGERIQHYMNYGSLIKFSRPGDYTYLGAS  
Hs 164 PSVGLSD--ISITFSASVPLAA--IDDEHIEKDYHSEYHETKLDGEFHQHH--GVYKFSRNGYHYTQHGAS  
At 210 RHOHR--QDLVGVKAVPOLAMHLDNAAWVGGKDVAECKFDGRICHHN--GDTYFSRNEFDHESYAHM

Sc 317 LSGAL--OHLRFETDSKECILDGEMTDAKRRVIPFGLVKGSAPFALSFSNSNVDCHPLVYVEDLYNGTSLTP  
Hs 239 PEGVLPFIHNAEKADIQICILDGEMTAPNTTTFQKGRKFK--F--MEDSCLTCYCVEDVIMVNNKKLGE  
At 286 SDLIVQ-----ILVD--KCILDGEMVDTSTIRFAEFGNQIARAE--EGLDSHKLCYSAEDVLYVGDTSIF

Sc 395 LPLQRYVYLSNIPPLNIEIVRS-----RCYVESKPSLEVALSLGSEGVLKYNSSYNVVSE  
Hs 313 EILKPYELSSIEPFGREIVQK-----AOHTKNVIDALNEATKKEGILKQPLSIYKEDKF  
At 355 QLYFERNELKKKPKPLKGRLEAVPEGGLNVHRPSGEPSSWSIVVHAALVEFFKETENREGIVLRDLESKEEEDP

Sc 459 NNNWRKPEYEEFGNLDKVRIGRDSGRKDSFMLGLLVLDEEYKKHQDSSEIVDHSQENHIONSRRVKKTIISFC  
Hs 377 GEGWRKPEYSGLMVLDLITGGYGGGS-----RGGVSHFLCAFAENPPPGESV--FHILS  
At 435 SGKWRKPEYR-AGALDLIIGGYGSGR-----RGGEVQFLVLAFAEAENVYPR--FISFC

Sc 539 SANGSQEFKIDRFTGHVK--TSEVAPPASILEFG--SKIPAEWILPSESILEIKSRSLDNTETNMQYATNC  
Hs 438 RVGGCMKEIYGLKLAKYWP-FHRKAPSSILCGT--EPPVIL-PCNSLLOH--AAETPSIYRTGL  
At 495 RVGGLSDLEINTVSKLPVPSNEHPKAPPSFYQVTHSKEPVWILSPEKSIITITS--DIRTFRSIVAPY

Sc 614 TLYGGYCKTRYDKWTCYTLADLYESFTVRKNPQYOAERSQLG-----LIRKKRKLISDSFHOIRKQLPSNIF  
Hs 508 TLRFPRIKIRDDKEWHECTLDDLELRGKASGKLASKLYIGGDDEQEKRRKAPKVKIGTIEHLAPNINANK  
At 572 TLRFPRIKIRYDKPWHECDKAFVELVNSSNGTQOKOSESSTQDNKVNKSSKGEKRVNLSLPSFTICTDSATK

Sc 688 GLLFVLSEVETEDTGIRITALEKTIVEHGGKLYNAILKRHSIGVRLISCKTECKALIDRG--YDHPNVLL  
Hs 588 ISNIFEDFCVSGTDSQPPLENRIAEEGYLQNPQ-----PDTCYIAGSENVKNILSNKEDVPAWLL  
At 652 KESIFSNIIYFENVPRSHLETFRHMEVENGGFMSMENN-----SVTICIAAEEGIIYQAAKRO--DVHFSVLL

Sc 766 CIAYKLLLEENYCFNOKMRAVAERDCLGDSHENDSETKLSSKSQLSLPPMGELEIDSEVFPFLFLFSNR-  
Hs 662 CFKTSFEPWOPSMHNCPSSEHFAFYDCGDSYITDILNQLKEVSGIKVSNQOTPEEASLADLEYRYSWDCS  
At 725 CCSRNPELPYFHHDAERTLOLDENSDSYWDEGLEGLKQVLSNAKES--EDSKSIDYKELCPEKRWSC-

Sc 845 ---YAYVPRRKSEEDDIIIRKIKLEGGATDQOSLCNIIIPYDPFL---IDCNEHEKQIKASDTI-----  
Hs 742 PLSFRRHTVDSYAVINNSTNECTDAIKALERFCKVVSCLAEVSHVGGEDHSYADFKAFRTF-----  
At 802 ---PLSCCVYYPYSQTESTEEALLGIMAKRLMLELACQVNNLA-ASHLLAAEEPLDETIVSSESEMEKR

Sc 913 ---PKIAPVVAPEWVHSTENCQPEEDFPYNY-----  
Hs 816 ---KATFVKESVVTSID-CEQEEQY-----  
At 878 LLLKRIIVVSSHVLSIAE-EKLCEDVYTRPKYMEESDTEESDKSEHDTTEVASQGSQOTKEPASSKIAITSSRGR

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Fig. 3B

Sc -----  
Hs -----  
At 957 SNTRAVKRGSRSTNSLQRVQRRRGKQPSKISGDETEESDASEEKVSTRLS DIAETDSFG EAQRNSSRGKCAKRGKSRVG

Sc -----  
Hs -----  
At 1037 QTQRVQSRRGKKA AKIGGDESDENDEL DGNNVSADAE EGNAGRSVENEETREPDI AKYTESQQRDNTVAVEEALQDS

Sc -----  
Hs -----  
At 1117 RNAKTEMDMKEKLQIHEDPLQAMLMKMFPIPSQKTTETSNRTTGEYRKANVS GECESESSEKRK LDAETDNTSVNAGAESDV

Sc -----  
Hs -----  
At 1197 VPPLVKKKKVS YRDVAGELLKDW

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Fig. 4

Sc 1 MDYPDP-D---TIRILITDNIHGYNENFPTGDDSXTFHEEMLAKNNHVLMAQSGLFHVNKPSFELYQVLKTLR  
Hs 1 MSTADALDDENITFVLVATDILHGLMEKDAARGNDIEVILBEIERLAQENEVDILLGGDLFHENKPSRKTILHTCLETLR  
At 1 MSREDFSD---TIRFLVATDCHLGYMEKDEIRRHDSFKAETICTSAEEKSVDEILLGGDLFHENKPSPTTLVKALETLR

Sc 77 LCCMGDKFCLELSDPSQVHHDEFTSVNYEDPNFNISIPVFGISGNHDDASGDSLLCPDILHATGLNHFGRKE--  
Hs 81 FYCMGDRPVQFEALSQSVNFGSKPEWVNYDCMNNISIPVFSIHGNHDDPGACALCAPDILSCAGFVNHFGRSSES--  
At 78 HCHNDKPVQFLLSDQVNEQN-AEGVNYEDERENGEPVFSIHGNHDDPAGVGNLSADILSACNLVNYEGRSLLGG

Sc 155 --SKIKIVPELFFQGSTNIALYGLFAVRDERLIRTKD-GVTFEEVTFRE---GWFNLCYHONHGHNTATFIFE  
Hs 159 --VKIDISPVLFFQGSTKIALYGLGSIPTDERLIRMEVN-KVTMRPKED---NSWFNLFVHQNRRKHGSTNFIFP  
At 157 SGVGGTTLPELFFQGSTTIALYGLGNIRDERLIRMEVQTPLEVOVTRPFCQEGCDVSWFNFVHQNRRVSNPKNAISF

Sc 228 QFLDFELDFVINGHEHECPNLVKNPIKNEFLOPGSSVATSLCSEAOPKYVFELIIRYGEAPMTPIPLETPTFRMK  
Hs 232 QFLDDFIDVINGHEHECKIAPTNEQQLFVLOPGSSVATSLSPGEAVKKHVGLLRK-GRKMNHKIPLHTVFOFFME  
At 237 HFLERFLDFVINGHEHECLIDQEVSGMGFHILOPGSSVATSLIGEPKPKHVLLIIF-GNOYPTPIPLTVRPFYET

Sc 308 STSLQVPHL-RPHL---KDATSKLLEQVEEMIRDANEETFOFLDDGEGDMVAEPKPLRLRVLDYSAPSNTQSPIDF  
Hs 311 LIVLAHPDIFNPDHPKVTATQSTCEKKEENIENA---EEELNSH---EPKPLVRLRVLDYSG-----F  
At 316 LIVLKDESPI-DENL---QSTLEHLDKVVRNLEKA---EKAENRS---EKLPLVRVLDYSG-----F

Sc 384 QVENERRFSHFVGRVANGELQFVRRSPVTRSKKSGINGESSEDEVDVEKLFSESGGELEVTLVN---DLLNKLQI  
Hs 374 EPFSVLRFQKEVDRVANPKDIHFELREONEEG-EEINFGKLT---PSEGTLRVEDLVKQYFQTAEKNQDI  
At 373 MTINPQREGQKVGAVANPDILIESKASK-KGRSE-ANLDEERL---PEELNQONDEALV---AESNKE

Sc 460 SLLPEVGLNEAVKRFVDKDETAKEFSHEISNEVGILSTEEFLITDDADES-KALIKOVRANSVRPTP--PENN  
Hs 447 SLITERGGEAVQEFVDKIBNDATFELVKYLE-----KTE-ELKIRHIAE-EDKIDEEVRFRETQKN--INED  
At 438 ELLPVNDLDVALNFVAKDRLAFYSCVOYNLO-----ETRGALAKSDAKKFEEDDLILKVGECLEERLDRSTPTG

Sc 536 ---FAFNGNGLDSTRSSNREVRV-SPLITQSHEDNESRITISQESSKPTKPE---RVF---LAKKIP  
Hs 517 DE---RRESTRARALRSQESASAFSAD-DLMSDLAEQANDSDDISISATNKGRRG---RGRRGGRGONSAGG--  
At 512 SGLFSTLTSENLTGSSGIANASFDDDEDTQSGGLAPPTGRRSSANTLGRVPTRGF--GRKASAMROAT

Sc 602 -AFSDSTVIS-DAENELDNNDACQDVIDENDIM---VSTEEF-ASGLLNGRKTTKIRPASTK---ASRGGR  
Hs 591 -QRGRFSTTROQPSRNVTAKNSEVLDSDSDVEDIFFETSKTD-QRSTSSSKNIMOSQVSKGVDFEEDDDDDP  
At 590 LDSLLEFOS-ORSASAAAGAAKSASTIGEDDVSS---PSSEVPEDNKPDSSEDESTKKGRRPAPARGGR

Sc 674 NSRTP---NTFI---IGSLLAKR--K-----  
Hs 669 FMNTSS-LRNR--DIYLLALEN-MQETG-KMICYKL---FVY-SLRF  
At 666 SGTSKRGRKNSSSSLNRLLSKDDDEDEDEDEDEKKLNKSQPRVTRNMGALRR

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Fig. 5

Sc 1 -----MSAAYKSIQIGIRSFDSNDN-----TIEFGPLTLIVGMNGGKTTTIECLKYATIGDLPPNE-KGVFIHDEKAT  
Hs 1 MLIFSVRDMFAKMSILGSRSGIEDAKKQITFFSPLTLIVGPNAGAGKTTTIECLKYICTGDLPPFG-KGNFIHDEPKVA  
At 1 -----MSTEDKMLIKGIRSFDPENSN-----ETTFEPPLTLIVGANGAGKTTTIECLKVSCTGLLPPNARSCHFIHDPKVA

Sc 72 GERDRAQIKLAFTANGCNVITRNJOLMKNKTTTFKTEGOLVAINNS-GRSILSRSLEADATPLYLGVPKAIL  
Hs 80 QETDRAQIKLOEDVNGELIAVORSVCTQSKTEFKTEGVTRT-KE-GEKVLSSCAEDREMISSLGVSKAAIL  
At 73 GETDRAQIKLREKIAAGKDA-CIRSEFOLTQASMEKRAESVLOTINPHAGEKVCLSYRCALDREIPALGVSKAIL

Sc 151 EYVIFCHOEDSLNPLSEPSNLKKKFDIFQAMTKKALNLSSTKMSVTHLLKOSFEHLKDKPKAKPLSTHGLC  
Hs 158 NNIVFCHOEDSNWPLSEKALKKQKDEIFSATRYIKALETLQAPOTQOKFEEOVELKYLNQYKFACEKRCITPSK  
At 153 ENVIVFVHQESNWPLOPSTLKKKFDIFSATRYTKALEVFKKAKNDQOQIKHTEKLENLQTLKDAAYKERESTAGOC

Sc 231 TTEYOYNEEVSHEPOLNETTESDKKFSNODFORILSKVENLKNITLES-DCVRLSNSIDHLLKPKPLNLANE  
Hs 238 AQVTSSKETVKSyenELDPKKNKNEFEENSKMKLONEKALDSRKQKEDKSELEBKKEKFGQTDQOLNLYNH  
At 233 ESTESSKVOLEKESSEKDAEENKEMMKDKERKLODOVSIXTAESEKFRICQOYAAPEENEDTIELKWKSK

Sc 310 SVVLMKNNQLRDEETSSIKDRSSLSLSNSLRROGELLAGRETYEKN-FNELSKKEAOKFOGLSNIENSDMA  
Hs 318 QETMRKEREKLVCHREDEKINKESRLLEKSELTEGQLCLOANRQEHIFARDSLIGSLATOLELQGFERGFSE  
At 313 EERLALLGTRKEREVDTETTSSILHAKNYLITSLCTEAFHMLLKNERDSALCNFFHYNLGNVSTEFSTE

Sc 389 QVNHEMSQKAFESDLTDIDQFAKLIQKETNLSDLKSIITVDSQNEY-NKDKSEKCHDS--ESLAENLKSEKSL  
Hs 398 QKKNFKHLKERO-EGEAKTACLMNDFAKETLQKQOLIEIRDRKGLER-IIELESEKSKNENLNYLQOLEG  
At 393 VVLGLTNRESRAGELEMLDKKKSSETALSTAWDCYELANDRWETIESOKRADEIRIGISRIENENERSSEFEY

Sc 466 MODSNHELENLKYTERKQSWESSEIKPKLNQKIEENENIIEENQIENEFDRIMKTNOADLYARKGTTKKSINTKL  
Hs 476 SADRLELDELILKAERELSKAENSNBETLKMEISLONEKADLITTEKRDQETQNHHTTTFQEFATDEKDED  
At 473 SEVDKOTDERENQVQVLEKTKNSERGFESITKCHETYSLEKIKITNREREVNAGDAED-LITRIDECKDRIR

Sc 546 FEOKITEFLODSRIQAFPLTCEORALEMOCOLFINMORNAINNKHEHLDRYTNALYNLNTIEKLODNQKS  
Hs 556 EOTKIKSHSD-----ETSLGYPNKKOLELSSKS---KEINQTRDLAKLNELASSEONKNHINNELERKEEQ  
At 552 GVLGRLPPEKD-----MKREYCALRSIRBYDDLSKS---EAEKEVNMLOMKIQEYNS--LFFKHNKDTESRYI

Sc 626 KERHIOILSENPEPCTIDYNDLEETELSYNTALENLKMTTLEFNVALIAERDSCCYKSRKFE--NESFKSKL  
Hs 628 LSSYEDKLFVCGSQDRESILRKEETEKSSORAMLACATAYSQFITOLTENQS--CCFVOCVFOTEALQEAIS  
At 622 ESKOALKQESSTIDAPKLLSARKEKRDREYNMANGMROLEPFEKARQHS---CECCERSFT-ADBEASTIK

Sc 704 LOEYKTFDINFELKDTQONEKEYLHSLRLKHHIINNSN-EKIDNSOCLKAKETKTSKSKLDEEVDSTME  
Hs 706 DLQSKLLAPILKTESEKKEKRRDEELGAPARQIDLKEKEIFELRNKLONVNRQORLANDQESTLQTIM  
At 697 KORRASSTELKALAVESSNASVFOQDKRAFEEYSKLTTEIIELEAETLQCHTEELGOKSEALDILGSSQTH

Sc 783 DEKELAESEREIEKFTYEKELKDENSSKTSEELSIYNTSDGICTVDELDQOQSMNDLELRKTESDLOEKE  
Hs 786 PEESAKVC-TD-TIMRFOMELKDEKIAQAAKLOG-IDLETFQVNOEOKOKLDESSKELNPKLIQOQ  
At 777 ADKASIEALQOB-LENARLFQEVSYQLOEDMEYKLDFRGLGVATDESELSSLSKSKLGELEKREDDQYME

Sc 863 EKVRENSRMNLKKEKLTSELESSATOKNTSRSKRENDDSRVKALEARISIKNKEEAOQSVLAKYNER  
Hs 864 EOIOHLKSTTNEKSEKQSTNLORROQ---EEQTVELSTESSLYRINKAKEQSELETTLEKFOKKEINEN  
At 856 RDISCLQARWHADEKAKAMLRDTK---AEDDERLAEKSOLDLVVYLTBAGFLSKEREOLLSYNEFTIRN

Sc 943 IQVNNKKTADIRLRFQTIYNVDFEAGFDELQTTIKLELNE-----AQMLELKEOLELKSNEENEEKRKAD  
Hs 941 TSNIAQKENDIKEKVKNHGYMKIEHQDGDYMKQETSK-----VIAQISECEKKEKENEERLMDQDOT  
At 933 QEYEELAKKRYQOEVAHLKASYKINCFTFYDLKKGELLDQKORLSDQLOSCAENHAGEBURNDLRN

Sc 1018 SNPEENLKNLELIELSLOHIESETSLVONN-EERDKYQESSELRTRFEILSSENAGKLGKQOLNODSLT  
Hs 1017 CKIOERWLODNLTLRKNNEELKEEEGKOLKKE-OMOLOKSEHONLEENINIKRNHMLALGRONGYEEIIEF  
At 1013 QDLRRNEDNLNYRTTAKKEETRETESLEOOLNIECAAEAEIENILRREDEILSELNRCRTSVYESSISN

Sc 1097 LR-TDYKDIEKNYKEWELQTRSFVTDIDVYSKALDSAIMKFGKNNINIIDELWARTYSCTDIDTIKIRSD  
Hs 1096 KELREPCDABERYEMIVETTELKNDLDYYNLDQAIMKFKMKNEINKITRLWASTYRGODIYIEIRSDA  
At 1093 VELQOAYKDIKKEHFOXTOLTTTEANKOLDRYNALDKALVPHMKNEINKITIRELWOOTYRGODIYIISDS

Sc 1176 VS---SVVKGFSYNYRVVMYKQDVELDMRGCSAGQVSLIIRLALFETGANCGLALDEPTTNLDENIESLAI  
Hs 1176 ENVSALDARRNYNYRVVMKGDALDMRGCSAGQVSLIIRLALAETFCNLGGIALDEPTTNLDRENIESLAI  
At 1173 LG-----AGTRSYSYVMOTGDTELEMRGCSAGQVSLIIRLALAETFCNLGGIALDEPTTNLDGPNSESAGAI

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Fig. 6

		1		50
At	(1)	-----MIGVDSKSSSTTFLETMVESEKTKHTC		
Hs	(1)	-----MERKISR		
Sc	(1)	MSQLTEFISCIPVNEEQNEEDERGLCKIQIEDGAMLETLDENSLSGTRI		
Consensus	(1)		IETL E SKIS	
		51		100
At	(28)	LRLEISGADPIFVKGTWHN---SRFDISVTDGSSS-----		
Hs	(8)	IHLVSEPSITHFLQVSWEKTLESCEVITLTUGHSA-----		
Sc	(51)	EKMLYSEG TGIFSKSSTGINDLRIFTGENIDEESKKYVWYELLKMLTGHK		
Consensus	(51)	IKLLIS A IFLK SW S F ISLTDG SA		
		101		150
At	(60)	-----WICNATEEVAERAAQWDQPVSEYL-KLAEQYLGFO		
Hs	(43)	-----WTGTVSESEISQEADDMAMEKGKYVGE LRKALLSGA		
Sc	(101)	VYIASLDEKVVFTKWTICRMQDDEVWKVVMELLES---SAITRKLAELTTHPV		
Consensus	(101)		WTC MSEDEVA A DLD S YI KLAEL	
		151		200
At	(95)	QPNVSYSFSDALEGSKRTISWTFEKEGTHKLEWRWKCKPSTDSKKLTVGILLD		
Hs	(79)	GPADVYTFNFESKESCYFFFEKNLKDVSFRLGSFNLEKVENPAEVIRELIC		
Sc	(149)	KKGETDLFEMADKLYKDICCVDNSYRNKESDSSNRNRVQLARERELLDD		
Consensus	(151)	PADVYSF A E K I NDKD S KE F K DD I RELLD		
		201		250
At	(145)	FLMEANIRLSEEVYNKTR-SFEKMRSEAERCLAQGEKLCDEKTEFESATY		
Hs	(129)	YCLDTIAENQAKNEHLOK-ENERLLRDWNDVQGRFEKCVSAKEALETDLY		
Sc	(199)	KLETRDERTRAMVTLLENEKKKKRELHELLRONNIKLSDDVDLSALI		
Consensus	(201)	FLLET E S MM K E EKLIRE DILAQ EK LSDKD LESALY		
		251		300
At	(194)	----AKFLSVLNA--KKAKLR-----ALRDKEDSVRVVEE-----		
Hs	(178)	----KFFILVLNE--KTKIR-----SLHNKLLNAAQEREKDIKQEGE		
Sc	(249)	NTEVOKPISELNSPGKMRRTKTVVEPONLOKKLKDTSRRRANRKISNQS		
Consensus	(251)	KFISVLNA KK KIR AL KL A RE		
		301		350
At	(223)	-----EESTDKAESFEESGRSDDEKSEEEASKKATSSKARGGKRAARS---		
Hs	(215)	TAICSEMTADRDVPYDESTDDESENQTDLSGLASAAVSKDDSIISLSDVT		
Sc	(299)	VIKMEDDDFDDFOFFGLSKRPIITAKDKLSEKYDDITSFGDDTQSISFES		
Consensus	(301)	EDS DK FD SK DD A DDL S KASAA SKGD S S S		
		351		400
At	(265)	-----		
Hs	(265)	DIAPSRKRRORMQNLGTEPKMAPQENLOEKEKPDSSLPETSKKEHISA		
Sc	(349)	DSSSDVQKHLVSLDNGIQISAGRSDEYDGISGSESETDASAGEKKSSN		
Consensus	(351)	D A K G A D D DS SA S		
		401		423
At	(265)	-----		
Hs	(315)	ENMSLETLRNSSPEDLFEI---		
Sc	(399)	HSEQSGNDREPCLOTESETDIET		
Consensus	(401)	R D		